

# SEQUENCE LISTING

<110> Novartis AG  
 <120> ANTIBODY (11C7) ANTI NOGO A AND ITS PHARMACEUTICAL USE  
 <130> 4-32761P1/UNZ  
 <140> US/10/538,201  
 <141> 2006-03-08  
 <150> PCT/EP03/13960  
 <151> 2003-12-09  
 <150> UK 0228832.2  
 <151> 2002-10-12  
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 Trp Ile Gly Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro  
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 Ser Leu Lys Asp Lys Phe Ile Ile Ser Arg Asp Asn Ala Lys Asn Thr  
 85 90 95  
 Leu Tyr Leu Gln Val Ser Thr Val Arg Ser Glu Asp Thr Ala Leu Tyr  
 100 105 110  
 Tyr Cys Val Arg Pro Val Trp Met Tyr Ala Met Asp Tyr Trp Gly Gln  
 115 120 125  
 Gly Thr Ser Val Thr Val Ser Ser Ala Lys Thr Thr Pro Pro Ser Val  
 130 135 140  
 Tyr Pro Leu Ala Pro Gly Ser Ala Ala Gln Thr Asn Ser Met Val Thr  
 145 150 155 160  
 Leu Gly Cys Leu Val Lys Gly Tyr Phe Pro Glu Pro Val Thr Val Thr  
 165 170 175  
 Trp Asn Ser Gly Ser Leu Ser Ser Gly Val His Thr Phe Pro Ala Val  
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Thr Ile Gly Gln Pro Ala Ser Ile Ser Cys Lys Ser Ser Gln Ser Leu  
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 Leu His Ser Asp Gly Lys Thr Tyr Leu Asn Trp Leu Leu Gln Arg Pro  
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 Gly Gln Ser Pro Lys Arg Leu Ile Tyr Leu Val Ser Lys Leu Asp Ser  
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 Gly Val Pro Asp Arg Phe Thr Gly Ser Gly Ser Gly Thr Asp Phe Thr  
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 Trp Gln Gly Thr His Phe Pro Gln Thr Phe Gly Gly Gly Thr Lys Leu  
 115 120 125  
 Glu Ile Lys Arg Ala Asp Ala Ala Pro Thr Val Ser Ile Phe Pro Pro  
 130 135 140  
 Ser Ser Glu Gln Leu Thr Ser Gly Gly Ala Ser Val Val Cys Phe Leu  
 145 150 155 160  
 Asn Asn Phe Tyr Pro Lys Asp Ile Asn Val Lys Trp Lys Ile Asp Gly  
 165 170 175  
 Ser Glu Arg Gln Asn Gly Val Leu Asn Ser Trp Thr Asp Gln Asp Ser  
 180 185 190  
 Lys Asp Ser Thr Tyr Ser Met Ser Ser Thr Leu Thr Leu Thr Lys Asp  
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cct Pro 145	cct Pro	ccc Pro	ccg Pro	gcc Ala	agc Ser 150	gtg Val	agc Ser	ccc Pro	cag Gln 155	gca Ala	gag Glu	ccc Pro	gtg Val	tgg Trp	acc Thr 160	480	
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cct Pro	gct Ala	gca Ala 195	tct Ser	gag Glu	cct Pro	gtg Val	ata Ile 200	cgc Arg	tcc Ser	tct Ser	gca Ala 205	gaa Glu 205	aat Asn	atg Met	gac Asp	624	
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cca Pro 225	tct Ser	gtc Val	ctg Leu	ctt Leu	gaa Glu 230	act Thr	gct Ala	gct Ala	tct Ser	ctt Leu 235	cct Pro	tct Ser	ctg Leu	tct Ser	cct Pro 240	720	
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aca gta tta ccc act gaa gga aca ctt caa gaa aat gtc agt gaa gct Thr Val Leu Pro 260 Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala	816
tct aaa gag gtc tca gag aag gca aaa act cta ctc ata gat aga gat Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile 285 Asp Arg Asp	864
tta aca gag ttt tca gaa tta gaa tac tca gaa atg gga tca tcg ttc Leu Thr 290 Glu Phe Ser Glu Leu 295 Glu Tyr Ser Glu Met 300 Gly Ser Ser Phe	912
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gaa agt aaa gtg gat aaa aaa tgt ttt gca gat agc ctt gag caa act Glu Ser Lys Val 420 Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr	1296
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Lys	Thr	Ser 515	Asn	Pro	Phe	Leu	Val 520	Ala	Ala	Gln	Asp	Ser 525	Glu	Thr	Asp	
tat Tyr	gtc Val 530	aca Thr	aca Thr	gat Asp	aat Asn	tta Leu 535	aca Thr	aag Lys	gtg Val	act Thr	gag Glu 540	gaa Glu	gtc Val	gtg Val	gca Ala	1632
aac Asn 545	atg Met	cct Pro	gaa Glu	ggc Gly	ctg Leu 550	act Thr	cca Pro	gat Asp	tta Leu	gta Val 555	cag Gln	gaa Glu	gca Ala	tgt Cys	gaa Glu 560	1680
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cct Pro 625	agt Ser	gct Ala	ggg Gly	gct Ala	tcc Ser 630	gtg Val	ata Ile	cag Gln	ccc Pro	agc Ser 635	tca Ser	tca Ser	cca Pro	tta Leu	gaa Glu 640	1920
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cca Pro	cca Pro	tat Tyr	gaa Glu 660	gag Glu	gcc Ala	atg Met	agt Ser	gta Val 665	tca Ser	cta Leu	aaa Lys	aaa Lys	gta Val 670	tca Ser	gga Gly	2016
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 35 40 45  
 Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly Leu Ser  
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 Ala Ala Pro Val Pro Thr Ala Pro Ala Ala Gly Ala Pro Leu Met Asp  
 65 70 75 80  
 Phe Gly Asn Asp Phe Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala  
 85 90 95  
 Ala Pro Pro Val Ala Pro Glu Arg Gln Pro Ser Trp Asp Pro Ser Pro  
 100 105 110  
 Val Ser Ser Thr Val Pro Ala Pro Ser Pro Leu Ser Ala Ala Ala Val  
 115 120 125  
 Ser Pro Ser Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro  
 130 135 140  
 Pro Pro Pro Pro Ala Ser Val Ser Pro Gln Ala Glu Pro Val Trp Thr  
 145 150 155 160  
 Pro Pro Ala Pro Ala Pro Ala Ala Pro Pro Ser Thr Pro Ala Ala Pro  
 165 170 175  
 Lys Arg Arg Gly Ser Ser Gly Ser Val Asp Glu Thr Leu Phe Ala Leu  
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 195 200 205  
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 Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro Ser Leu Ser Pro  
 225 230 235 240  
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 245 250 255  
 Thr Val Leu Pro Thr Glu Gly Thr Leu Gln Glu Asn Val Ser Glu Ala  
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Ser Lys Glu Val Ser Glu Lys Ala Lys Thr Leu Leu Ile Asp Arg Asp  
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Leu Thr Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met Gly Ser Ser Phe  
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Ser Val Ser Pro Lys Ala Glu Ser Ala Val Ile Val Ala Asn Pro Arg  
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Asn Asn Ile Leu His Asn Gln Gln Glu Leu Pro Thr Ala Leu Thr Lys  
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Leu Val Lys Glu Asp Glu Val Val Ser Ser Glu Lys Ala Lys Asp Ser  
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Phe Asn Glu Lys Arg Val Ala Val Glu Ala Pro Met Arg Glu Glu Tyr  
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Ala Asp Phe Lys Pro Phe Glu Arg Val Trp Glu Val Lys Asp Ser Lys  
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Glu Asp Ser Asp Met Leu Ala Ala Gly Gly Lys Ile Glu Ser Asn Leu  
 405 410 415

Glu Ser Lys Val Asp Lys Lys Cys Phe Ala Asp Ser Leu Glu Gln Thr  
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Asn His Glu Lys Asp Ser Glu Ser Ser Asn Asp Asp Thr Ser Phe Pro  
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Ser Thr Pro Glu Gly Ile Lys Asp Arg Ser Gly Ala Tyr Ile Thr Cys  
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Ala Pro Phe Asn Pro Ala Ala Thr Glu Ser Ile Ala Thr Asn Ile Phe  
 465 470 475 480

Pro Leu Leu Gly Asp Pro Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys  
 485 490 495

Ile Glu Glu Lys Lys Ala Gln Ile Val Thr Glu Lys Asn Thr Ser Thr  
 500 505 510

Lys Thr Ser Asn Pro Phe Leu Val Ala Ala Gln Asp Ser Glu Thr Asp  
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Tyr Val Thr Thr Asp Asn Leu Thr Lys Val Thr Glu Glu Val Val Ala  
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Asn Met Pro Glu Gly Leu Thr Pro Asp Leu Val Gln Glu Ala Cys Glu  
 545 550 555 560

Ser Glu Leu Asn Glu Val Thr Gly Thr Lys Ile Ala Tyr Glu Thr Lys  
 565 570 575

Met Asp Leu Val Gln Thr Ser Glu Val Met Gln Glu Ser Leu Tyr Pro  
 580 585 590

Ala Ala Gln Leu Cys Pro Ser Phe Glu Glu Ser Glu Ala Thr Pro Ser  
 595 600 605

Pro Val Leu Pro Asp Ile Val Met Glu Ala Pro Leu Asn Ser Ala Val  
 610 615 620

Pro Ser Ala Gly Ala Ser Val Ile Gln Pro Ser Ser Ser Pro Leu Glu  
 625 630 635 640

Ala Ser Ser Val Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro  
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Pro Pro Tyr Glu Glu Ala Met Ser Val Ser Leu Lys Lys Val Ser Gly  
 660 665 670

Ile Lys Glu Glu Ile Lys Glu Pro Glu Asn Ile Asn Ala Ala Leu Gln  
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Glu Thr Glu Ala Pro Tyr Ile Ser Ile Ala Cys Asp Leu Ile Lys Glu  
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Thr Lys Leu Ser Ala Glu Pro Ala Pro Asp Phe Ser Asp Tyr Ser Glu  
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Met Ala Lys Val Glu Gln Pro Val Pro Asp His Ser Glu Leu Val Glu  
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Asp Ser Ser Pro Asp Ser Glu Pro Val Asp Leu Phe Ser Asp Asp Ser  
 740 745 750

Ile Pro Asp Val Pro Gln Lys Gln Asp Glu Thr Val Met Leu Val Lys  
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Glu Ser Leu Thr Glu Thr Ser Phe Glu Ser Met Ile Glu Tyr Glu Asn  
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Asp	Glu	Val	Ser	Thr	Leu	Ser	Lys	Lys	Glu	Lys	Ile	Pro	Leu	Gln	Met	
			820					825					830			
Glu	Glu	Leu	Ser	Thr	Ala	Val	Tyr	Ser	Asn	Asp	Asp	Leu	Phe	Ile	Ser	
		835					840					845				
Lys	Glu	Ala	Gln	Ile	Arg	Glu	Thr	Glu	Thr	Phe	Ser	Asp	Ser	Ser	Pro	
	850					855					860					
Ile	Glu	Ile	Ile	Asp	Glu	Phe	Pro	Thr	Leu	Ile	Ser	Ser	Lys	Thr	Asp	
865					870					875					880	
Ser	Phe	Ser	Lys	Leu	Ala	Arg	Glu	Tyr	Thr	Asp	Leu	Glu	Val	Ser	His	
				885					890					895		
Lys	Ser	Glu	Ile	Ala	Asn	Ala	Pro	Asp	Gly	Ala	Gly	Ser	Leu	Pro	Cys	
			900					905					910			
Thr	Glu	Leu	Pro	His	Asp	Leu	Ser	Leu	Lys	Asn	Ile	Gln	Pro	Lys	Val	
		915					920					925				
Glu	Glu	Lys	Ile	Ser	Phe	Ser	Asp	Asp	Phe	Ser	Lys	Asn	Gly	Ser	Ala	
	930					935					940					
Thr	Ser	Lys	Val	Leu	Leu	Leu	Pro	Pro	Asp	Val	Ser	Ala	Leu	Ala	Thr	
945				950						955					960	
Gln	Ala	Glu	Ile	Glu	Ser	Ile	Val	Lys	Pro	Lys	Val	Leu	Val	Lys	Glu	
				965					970					975		
Ala	Glu	Lys	Lys	Leu	Pro	Ser	Asp	Thr	Glu	Lys	Glu	Asp	Arg	Ser	Pro	
			980					985					990			
Ser	Ala	Ile	Phe	Ser	Ala	Glu	Leu	Ser	Lys	Thr	Ser	Val	Val	Asp	Leu	
		995					1000					1005				
Leu	Tyr	Trp	Arg	Asp	Ile	Lys	Lys	Thr	Gly	Val	Val	Phe	Gly	Ala		
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Ser	Leu	Phe	Leu	Leu	Leu	Ser	Leu	Thr	Val	Phe	Ser	Ile	Val	Ser		
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Val	Thr	Ala	Tyr	Ile	Ala	Leu	Ala	Leu	Leu	Ser	Val	Thr	Ile	Ser		
	1040					1045					1050					

Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser Asp  
1055 1060 1065

Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala Ile  
1070 1075 1080

Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His  
1085 1090 1095

Val Asn Cys Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val Asp  
1100 1105 1110

Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val Phe  
1115 1120 1125

Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile Leu  
1130 1135 1140

Ala Leu Ile Ser Leu Phe Ser Val Pro Val Ile Tyr Glu Arg His  
1145 1150 1155

Gln Ala Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Asn Val  
1160 1165 1170

Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu Lys  
1175 1180 1185

Arg Lys Ala Glu  
1190

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<212> PRT  
<213> Homo sapiens

<220>  
<221> PEPTIDE  
<222> (1)..(18)  
<223> Human NogoA\_623-640

<400> 6

Asn Tyr Glu Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu  
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Glu Ala

<210> 7  
<211> 819

<212> PRT  
<213> Homo sapiens

<220>  
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<222> (1)..(819)  
<223> human Nig

<400> 7

Asp Glu Thr Leu Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Arg  
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Ser Ser Ala Glu Asn Met Asp Leu Lys Glu Gln Pro Gly Asn Thr Ile  
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Ser Ala Gly Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala  
35 40 45

Ser Leu Pro Ser Leu Ser Pro Leu Ser Ala Ala Ser Phe Lys Glu His  
50 55 60

Glu Tyr Leu Gly Asn Leu Ser Thr Val Leu Pro Thr Glu Gly Thr Leu  
65 70 75 80

Gln Glu Asn Val Ser Glu Ala Ser Lys Glu Val Ser Glu Lys Ala Lys  
85 90 95

Thr Leu Leu Ile Asp Arg Asp Leu Thr Glu Phe Ser Glu Leu Glu Tyr  
100 105 110

Ser Glu Met Gly Ser Ser Phe Ser Val Ser Pro Lys Ala Glu Ser Ala  
115 120 125

Val Ile Val Ala Asn Pro Arg Glu Glu Ile Ile Val Lys Asn Lys Asp  
130 135 140

Glu Glu Glu Lys Leu Val Ser Asn Asn Ile Leu His Asn Gln Gln Glu  
145 150 155 160

Leu Pro Thr Ala Leu Thr Lys Leu Val Lys Glu Asp Glu Val Val Ser  
165 170 175

Ser Glu Lys Ala Lys Asp Ser Phe Asn Glu Lys Arg Val Ala Val Glu  
180 185 190

Ala Pro Met Arg Glu Glu Tyr Ala Asp Phe Lys Pro Phe Glu Arg Val  
195 200 205

Trp Glu Val Lys Asp Ser Lys Glu Asp Ser Asp Met Leu Ala Ala Gly  
210 215 220

Gly 225	Lys	Ile	Glu	Ser	Asn 230	Leu	Glu	Ser	Lys	Val 235	Asp	Lys	Lys	Cys	Phe 240
Ala	Asp	Ser	Leu	Glu 245	Gln	Thr	Asn	His	Glu 250	Lys	Asp	Ser	Glu	Ser 255	Ser
Asn	Asp	Asp	Thr 260	Ser	Phe	Pro	Ser	Thr 265	Pro	Glu	Gly	Ile	Lys 270	Asp	Arg
Ser	Gly	Ala 275	Tyr	Ile	Thr	Cys	Ala 280	Pro	Phe	Asn	Pro	Ala 285	Ala	Thr	Glu
Ser	Ile 290	Ala	Thr	Asn	Ile	Phe 295	Pro	Leu	Leu	Gly	Asp 300	Pro	Thr	Ser	Glu
Asn 305	Lys	Thr	Asp	Glu	Lys 310	Lys	Ile	Glu	Glu	Lys 315	Lys	Ala	Gln	Ile	Val 320
Thr	Glu	Lys	Asn	Thr 325	Ser	Thr	Lys	Thr	Ser 330	Asn	Pro	Phe	Leu	Val 335	Ala
Ala	Gln	Asp	Ser 340	Glu	Thr	Asp	Tyr	Val 345	Thr	Thr	Asp	Asn	Leu 350	Thr	Lys
Val	Thr	Glu 355	Glu	Val	Val	Ala	Asn 360	Met	Pro	Glu	Gly	Leu 365	Thr	Pro	Asp
Leu 370	Val	Gln	Glu	Ala	Cys	Glu 375	Ser	Glu	Leu	Asn	Glu 380	Val	Thr	Gly	Thr
Lys 385	Ile	Ala	Tyr	Glu	Thr 390	Lys	Met	Asp	Leu	Val 395	Gln	Thr	Ser	Glu	Val 400
Met	Gln	Glu	Ser	Leu 405	Tyr	Pro	Ala	Ala	Gln 410	Leu	Cys	Pro	Ser	Phe 415	Glu
Glu	Ser	Glu	Ala 420	Thr	Pro	Ser	Pro	Val 425	Leu	Pro	Asp	Ile	Val 430	Met	Glu
Ala	Pro	Leu 435	Asn	Ser	Ala	Val	Pro 440	Ser	Ala	Gly	Ala	Ser 445	Val	Ile	Gln
Pro	Ser 450	Ser	Ser	Pro	Leu	Glu 455	Ala	Ser	Ser	Val	Asn 460	Tyr	Glu	Ser	Ile
Lys 465	His	Glu	Pro	Glu	Asn 470	Pro	Pro	Pro	Tyr	Glu 475	Glu	Ala	Met	Ser	Val 480

Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu Pro Glu  
 485 490 495

Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile Ser Ile  
 500 505 510

Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro Ala Pro  
 515 520 525

Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro Val Pro  
 530 535 540

Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu Pro Val  
 545 550 555 560

Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys Gln Asp  
 565 570 575

Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr Ser Phe Glu  
 580 585 590

Ser Met Ile Glu Tyr Glu Asn Lys Glu Lys Leu Ser Ala Leu Pro Pro  
 595 600 605

Glu Gly Gly Lys Pro Tyr Leu Glu Ser Phe Lys Leu Ser Leu Asp Asn  
 610 615 620

Thr Lys Asp Thr Leu Leu Pro Asp Glu Val Ser Thr Leu Ser Lys Lys  
 625 630 635 640

Glu Lys Ile Pro Leu Gln Met Glu Glu Leu Ser Thr Ala Val Tyr Ser  
 645 650 655

Asn Asp Asp Leu Phe Ile Ser Lys Glu Ala Gln Ile Arg Glu Thr Glu  
 660 665 670

Thr Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr  
 675 680 685

Leu Ile Ser Ser Lys Thr Asp Ser Phe Ser Lys Leu Ala Arg Glu Tyr  
 690 695 700

Thr Asp Leu Glu Val Ser His Lys Ser Glu Ile Ala Asn Ala Pro Asp  
 705 710 715 720

Gly Ala Gly Ser Leu Pro Cys Thr Glu Leu Pro His Asp Leu Ser Leu  
 725 730 735



Lys Asn Ile Gln Pro Lys Val Glu Glu Lys Ile Ser Phe Ser Asp Asp  
740 745 750

Phe Ser Lys Asn Gly Ser Ala Thr Ser Lys Val Leu Leu Leu Pro Pro  
755 760 765

Asp Val Ser Ala Leu Ala Thr Gln Ala Glu Ile Glu Ser Ile Val Lys  
770 775 780

Pro Lys Val Leu Val Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr  
785 790 795 800

Glu Lys Glu Asp Arg Ser Pro Ser Ala Ile Phe Ser Ala Glu Leu Ser  
805 810 815

Lys Thr Ser

<210> 8  
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<212> PRT  
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<220>  
<221> BINDING  
<222> (1)..(10)  
<223> hypervariable part of heavy chain of 11C7

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Gly Phe Asp Phe Arg Arg Asn Trp Met Ser  
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<210> 9  
<211> 17  
<212> PRT  
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<220>  
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<400> 9

Glu Ile Asn Pro Asp Ser Ser Lys Ile Asn Tyr Thr Pro Ser Leu Lys  
1 5 10 15

Asp

<210> 10  
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<212> PRT

<213> Mus musculus

<220>

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<400> 10

Pro Val Trp Met Tyr Ala Met Asp Tyr  
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<210> 11

<211> 16

<212> PRT

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<220>

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<222> (1)..(16)

<223> hypervariable part of light chain of 11C7

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Lys Ser Ser Gln Ser Leu Leu His Ser Asp Gly Lys Thr Tyr Leu Asn  
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<210> 12

<211> 7

<212> PRT

<213> Mus musculus

<220>

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<222> (1)..(7)

<223> hypervariable part of light chain of 11C7

<400> 12

Leu Val Ser Lys Leu Asp Ser  
1 5

<210> 13

<211> 9

<212> PRT

<213> Mus musculus

<220>

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<222> (1)..(9)

<223> hypervariable part of light chain of 11C7

<400> 13

Trp Gln Gly Thr His Phe Pro Gln Thr  
1 5

<210> 14  
<211> 30  
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<220>  
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<223> DNA-CDR1-11C7

<400> 14  
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30

<210> 15  
<211> 51  
<212> DNA  
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<220>  
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<222> (1)..(51)  
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<400> 15  
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51

<210> 16  
<211> 27  
<212> DNA  
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<220>  
<221> misc\_binding  
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<223> DNA-CDR3-11C7

<400> 16  
ccggtctgga tgtatgctat ggactac

27

<210> 17  
<211> 48  
<212> DNA  
<213> Mus musculus

<220>  
<221> misc\_binding  
<222> (1)..(48)  
<223> DNA-CDR'1-11C7

<400> 17  
aagtcaagtc agagcctctt gcatagtgat ggaaagacat atttgaat

48

<210> 18  
<211> 21  
<212> DNA  
<213> Mus musculus

<220>  
 <221> misc\_binding  
 <222> (1)..(21)  
 <223> DNA-CDR'2-11C7  
  
 <400> 18  
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<210> 19  
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 <212> DNA  
 <213> Mus musculus

<220>  
 <221> misc\_binding  
 <222> (1)..(27)  
 <223> DNA-CDR'3-11C7  
  
 <400> 19  
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<210> 20  
 <211> 54  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)..(54)  
 <223> leader sequence for heavy chain of 11C7

<400> 20  
 atg gat ttt ggg ctg att ttt ttt att gtt ggt ctt tta aaa ggg gtc 48  
 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val  
 1 5 10 15  
  
 cag tgt 54  
 Gln Cys

<210> 21  
 <211> 18  
 <212> PRT  
 <213> Mus musculus

<400> 21  
 Met Asp Phe Gly Leu Ile Phe Phe Ile Val Gly Leu Leu Lys Gly Val  
 1 5 10 15  
  
 Gln Cys

<210> 22  
 <211> 57  
 <212> DNA  
 <213> Mus musculus

<220>  
 <221> CDS  
 <222> (1)..(57)  
 <223> leader sequence for 11C7-light chain

<400> 22  
 atg agt cct gcc cag ttc ctg ttt ctg tta gtg ctc tgg att cgg gaa 48  
 Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu  
 1 5 10 15  
 acc agc ggt 57  
 Thr Ser Gly

<210> 23  
 <211> 19  
 <212> PRT  
 <213> Mus musculus

<400> 23  
 Met Ser Pro Ala Gln Phe Leu Phe Leu Leu Val Leu Trp Ile Arg Glu  
 1 5 10 15  
 Thr Ser Gly

<210> 24  
 <211> 181  
 <212> PRT  
 <213> Homo sapiens

<220>  
 <221> PEPTIDE  
 <222> (1)..(181)  
 <223> human Nig-D20

<400> 24  
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 20 25 30  
 Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val  
 35 40 45  
 Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val  
 50 55 60  
 Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu  
 65 70 75 80

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met  
 85 90 95  
 Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu  
 100 105 110  
 Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile  
 115 120 125  
 Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro  
 130 135 140  
 Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro  
 145 150 155 160  
 Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu  
 165 170 175  
 Pro Val Asp Leu Phe  
 180

<210> 25  
 <211> 3492  
 <212> DNA  
 <213> Rattus norvegicus

<220>  
 <221> CDS  
 <222> (1)..(3492)  
 <223> rat NogoA

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gag gac gag gag gac gag gag gag gag gag gac gag gag gag gac gac Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp 35 40 45	144
gag gac cta gag gaa ctg gag gtg ctg gag agg aag ccc gca gcc ggg Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly 50 55 60	192
ctg tcc gca gct gcg gtg ccg ccc gcc gcc gcc gcc gcg ccg ctg ctg gac Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp 65 70 75 80	240
ttc agc agc gac tcg gtg ccc ccc gcg ccc cgc ggg ccg ctg ccg gcc Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala 85 90 95	288
gcg ccc cct gcc gct cct gag agg cag cca tcc tgg gaa cgc agc ccc	336

Ala	Pro	Pro	Ala 100	Ala	Pro	Glu	Arg	Gln 105	Pro	Ser	Trp	Glu	Arg 110	Ser	Pro	
gcg Ala	gcg Ala	ccc Pro 115	gcg Ala	cca Pro	tcc Ser	ctg Leu	ccg Pro 120	ccc Pro	gct Ala	gcc Ala	gca Ala	gtc Val 125	ctg Leu	ccc Pro	tcc Ser	384
aag Lys	ctc Leu 130	cca Pro	gag Glu	gac Asp	gac Asp	gag Glu 135	cct Pro	ccg Pro	gcg Ala	agg Arg	ccc Pro 140	ccg Pro	cct Pro	ccg Pro	ccg Pro	432
cca Pro 145	gcc Ala	ggc Gly	gcg Ala	agc Ser	ccc Pro 150	ctg Leu	gcg Ala	gag Glu	ccc Pro	gcc Ala 155	gcg Ala	ccc Pro	cct Pro	tcc Ser	acg Thr 160	480
ccg Pro	gcc Ala	gcg Ala	ccc Pro	aag Lys 165	cgc Arg	agg Arg	ggc Gly	tcc Ser	ggc Gly 170	tca Ser	gtg Val	gat Asp	gag Glu	acc Thr 175	ctt Leu	528
ttt Phe	gct Ala	ctt Leu	cct Pro 180	gct Ala	gca Ala	tct Ser	gag Glu	cct Pro 185	gtg Val	ata Ile	ccc Pro	tcc Ser	tct Ser 190	gca Ala	gaa Glu	576
aaa Lys	att Ile	atg Met 195	gat Asp	ttg Leu	atg Met	gag Glu	cag Gln 200	cca Pro	ggc Gly	aac Asn	act Thr	gtt Val 205	tcg Ser	tct Ser	ggc Gly	624
caa Gln	gag Glu 210	gat Asp	ttc Phe	cca Pro	tct Ser	gtc Val 215	ctg Leu	ctt Leu	gaa Glu	act Thr	gct Ala 220	gcc Ala	tct Ser	ctt Leu	cct Pro	672
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tta Leu	aac Asn	gaa Glu	gct Ala 260	tct Ser	aaa Lys	gag Glu	ttg Leu	cca Pro 265	gag Glu	agg Arg	gca Ala	aca Thr	aac Asn 270	cca Pro	ttt Phe	816
gta Val	aac Asn 275	aga Arg	gat Asp	tta Leu	gca Ala	gaa Glu	ttt Phe 280	tca Ser	gaa Glu	tta Leu	gaa Glu	tat Tyr 285	tca Ser	gaa Glu	atg Met	864
gga Gly	tca Ser 290	tct Ser	ttt Phe	aaa Lys	ggc Gly	tcc Ser 295	cca Pro	aaa Lys	gga Gly	gag Glu	tca Ser 300	gcc Ala	ata Ile	tta Leu	gta Val	912
gaa Glu 305	aac Asn	act Thr	aag Lys	gaa Glu	gaa Glu 310	gta Val	att Ile	gtg Val	agg Arg	agt Ser 315	aaa Lys	gac Asp	aaa Lys	gag Glu	gat Asp 320	960
tta Leu	gtt Val	tgt Cys	agt Ser	gca Ala 325	gcc Ala	ctt Leu	cac His	agt Ser	cca Pro 330	caa Gln	gaa Glu	tca Ser	cct Pro	gtg Val 335	ggc Gly	1008
aaa Lys	gaa Glu	gac Asp	aga Arg 340	gtt Val	gtg Val	tct Ser	cca Pro	gaa Glu 345	aag Lys	aca Thr	atg Met	gac Asp	att Ile 350	ttt Phe	aac Asn	1056
gaa Glu	atg Met	cag Gln	atg Met	tca Ser	gta Val	gta Val	gca Ala	cct Pro	gtg Val	agg Arg	gaa Glu	gag Glu	tat Tyr	gca Ala	gac Asp	1104

355				360				365								
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Phe	Lys	Pro	Phe	Glu	Gln	Ala	Trp	Glu	Val	Lys	Asp	Thr	Tyr	Glu	Gly	
	370					375					380					
agt	agg	gat	gtg	ctg	gct	gct	aga	gct	aat	gtg	gaa	agt	aaa	gtg	gac	1200
Ser	Arg	Asp	Val	Leu	Ala	Ala	Arg	Ala	Asn	Val	Glu	Ser	Lys	Val	Asp	
	385				390					395					400	
aga	aaa	tgc	ttg	gaa	gat	agc	ctg	gag	caa	aaa	agt	ctt	ggg	aag	gat	1248
Arg	Lys	Cys	Leu	Glu	Asp	Ser	Leu	Glu	Gln	Lys	Ser	Leu	Gly	Lys	Asp	
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agt	gaa	ggc	aga	aat	gag	gat	gct	tct	ttc	ccc	agt	acc	cca	gaa	cct	1296
Ser	Glu	Gly	Arg	Asn	Glu	Asp	Ala	Ser	Phe	Pro	Ser	Thr	Pro	Glu	Pro	
			420					425					430			
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Val	Lys	Asp	Ser	Ser	Arg	Ala	Tyr	Ile	Thr	Cys	Ala	Ser	Phe	Thr	Ser	
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Ala	Thr	Glu	Ser	Thr	Thr	Ala	Asn	Thr	Phe	Pro	Leu	Leu	Glu	Asp	His	
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act	tca	gaa	aat	aaa	aca	gat	gaa	aaa	aaa	ata	gaa	gaa	agg	aag	gcc	1440
Thr	Ser	Glu	Asn	Lys	Thr	Asp	Glu	Lys	Lys	Ile	Glu	Glu	Arg	Lys	Ala	
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caa	att	ata	aca	gag	aag	act	agc	ccc	aaa	acg	tca	aat	cct	ttc	ctt	1488
Gln	Ile	Ile	Thr	Glu	Lys	Thr	Ser	Pro	Lys	Thr	Ser	Asn	Pro	Phe	Leu	
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gta	gca	gta	cag	gat	tct	gag	gca	gat	tat	gtt	aca	aca	gat	acc	tta	1536
Val	Ala	Val	Gln	Asp	Ser	Glu	Ala	Asp	Tyr	Val	Thr	Thr	Asp	Thr	Leu	
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Ser	Lys	Val	Thr	Glu	Ala	Ala	Val	Ser	Asn	Met	Pro	Glu	Gly	Leu	Thr	
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Pro	Asp	Leu	Val	Gln	Glu	Ala	Cys	Glu	Ser	Glu	Leu	Asn	Glu	Ala	Thr	
	530					535					540					
ggc	aca	aag	att	gct	tat	gaa	aca	aaa	gtg	gac	ttg	gtc	caa	aca	tca	1680
Gly	Thr	Lys	Ile	Ala	Tyr	Glu	Thr	Lys	Val	Asp	Leu	Val	Gln	Thr	Ser	
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Glu	Ala	Ile	Gln	Glu	Ser	Leu	Tyr	Pro	Thr	Ala	Gln	Leu	Cys	Pro	Ser	
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Phe	Glu	Glu	Ala	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val	
			580					585					590			
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Met	Glu	Ala	Pro	Leu	Asn	Ser	Leu	Leu	Pro	Ser	Ala	Gly	Ala	Ser	Val	
		595					600					605				
gtg	cag	ccc	agt	gta	tcc	cca	ctg	gaa	gca	cct	cct	cca	gtt	agt	tat	1872
Val	Gln	Pro	Ser	Val	Ser	Pro	Leu	Glu	Ala	Pro	Pro	Pro	Val	Ser	Tyr	
	610					615					620					



gac Asp 625	agt Ser	ata Ile	aag Lys	ctt Leu	gag Glu 630	cct Pro	gaa Glu	aac Asn	ccc Pro	cca Pro 635	cca Pro	tat Tyr	gaa Glu	gaa Glu	gcc Ala 640	1920
atg Met	aat Asn	gta Val	gca Ala	cta Leu 645	aaa Lys	gct Ala	ttg Leu	gga Gly	aca Thr 650	aag Lys	gaa Glu	gga Gly	ata Ile	aaa Lys 655	gag Glu	1968
cct Pro	gaa Glu	agt Ser	ttt Phe 660	aat Asn	gca Ala	gct Ala	gtt Val	cag Gln 665	gaa Glu	aca Thr	gaa Glu	gct Ala	cct Pro 670	tat Tyr	ata Ile	2016
tcc Ser	att Ile	gcg Ala 675	tgt Cys	gat Asp	tta Leu	att Ile	aaa Lys 680	gaa Glu	aca Thr	aag Lys	ctc Leu	tcc Ser 685	act Thr	gag Glu	cca Pro	2064
agt Ser	cca Pro 690	gat Asp	ttc Phe	tct Ser	aat Asn	tat Tyr 695	tca Ser	gaa Glu	ata Ile	gca Ala	aaa Lys 700	ttc Phe	gag Glu	aag Lys	tcg Ser	2112
gtg Val 705	ccc Pro	gaa Glu	cac His	gct Ala	gag Glu 710	cta Leu	gtg Val	gag Glu	gat Asp	tcc Ser 715	tca Ser	cct Pro	gaa Glu	tct Ser	gaa Glu 720	2160
cca Pro	gtt Val	gac Asp	tta Leu	ttt Phe 725	agt Ser	gat Asp	gat Asp	tcg Ser	att Ile 730	cct Pro	gaa Glu	gtc Val	cca Pro	caa Gln 735	aca Thr	2208
caa Gln	gag Glu	gag Glu	gct Ala 740	gtg Val	atg Met	ctc Leu	atg Met	aag Lys 745	gag Glu	agt Ser	ctc Leu	act Thr	gaa Glu 750	gtg Val	tct Ser	2256
gag Glu	aca Thr 755	gta Val	gcc Ala	cag Gln	cac His	aaa Lys	gag Glu 760	gag Glu	aga Arg	ctt Leu	agt Ser	gcc Ala 765	tca Ser	cct Pro	cag Gln	2304
gag Glu 770	cta Leu	gga Gly	aag Lys	cca Pro	tat Tyr	tta Leu 775	gag Glu	tct Ser	ttt Phe	cag Gln	ccc Pro 780	aat Asn	tta Leu	cat His	agt Ser	2352
aca Thr 785	aaa Lys	gat Asp	gct Ala	gca Ala	tct Ser 790	aat Asn	gac Asp	att Ile	cca Pro	aca Thr 795	ttg Leu	acc Thr	aaa Lys	aag Lys	gag Glu 800	2400
aaa Lys	att Ile	tct Ser	ttg Leu	caa Gln 805	atg Met	gaa Glu	gag Glu	ttt Phe	aat Asn 810	act Thr	gca Ala	att Ile	tat Tyr	tca Ser 815	aat Asn	2448
gat Asp	gac Asp	tta Leu	ctt Leu 820	tct Ser	tct Ser	aag Lys	gaa Glu	gac Asp 825	aaa Lys	ata Ile	aaa Lys	gaa Glu	agt Ser 830	gaa Glu	aca Thr	2496
ttt Phe	tca Ser	gat Asp 835	tca Ser	tct Ser	ccg Pro	att Ile	gag Glu 840	ata Ile	ata Ile	gat Asp	gaa Glu	ttt Phe 845	ccc Pro	acg Thr	ttt Phe	2544
gtc Val	agt Ser 850	gct Ala	aaa Lys	gat Asp	gat Asp	tct Ser 855	cct Pro	aaa Lys	tta Leu	gcc Ala	aag Lys 860	gag Glu	tac Tyr	act Thr	gat Asp	2592
cta Leu 865	gaa Glu	gta Val	tcc Ser	gac Asp	aaa Lys 870	agt Ser	gaa Glu	att Ile	gct Ala	aat Asn 875	atc Ile	caa Gln	agc Ser	ggg Gly	gca Ala 880	2640

gat tca ttg cct tgc tta gaa ttg ccc tgt gac ctt tct ttc aag aat	2688
Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn	
885 890 895	
ata tat cct aaa gat gaa gta cat gtt tca gat gaa ttc tcc gaa aat	2736
Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn	
900 905 910	
agg tcc agt gta tct aag gca tcc ata tcg cct tca aat gtc tct gct	2784
Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala	
915 920 925	
ttg gaa cct cag aca gaa atg ggc agc ata gtt aaa tcc aaa tca ctt	2832
Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu	
930 935 940	
acg aaa gaa gca gag aaa aaa ctt cct tct gac aca gag aaa gag gac	2880
Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp	
945 950 955 960	
aga tcc ctg tca gct gta ttg tca gca gag ctg agt aaa act tca gtt	2928
Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val	
965 970 975	
gtt gac ctc ctc tac tgg aga gac att aag aag act gga gtg gtg ttt	2976
Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe	
980 985 990	
ggt gcc agc tta ttc ctg ctg ctg tct ctg aca gtg ttc agc att gtc	3024
Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val	
995 1000 1005	
agt gta acg gcc tac att gcc ttg gcc ctg ctc tcg gtg act atc	3069
Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile	
1010 1015 1020	
agc ttt agg ata tat aag ggc gtg atc cag gct atc cag aaa tca	3114
Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser	
1025 1030 1035	
gat gaa ggc cac cca ttc agg gca tat tta gaa tct gaa gtt gct	3159
Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala	
1040 1045 1050	
ata tca gag gaa ttg gtt cag aaa tac agt aat tct gct ctt ggt	3204
Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly	
1055 1060 1065	
cat gtg aac agc aca ata aaa gaa ctg agg cgg ctt ttc tta gtt	3249
His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val	
1070 1075 1080	
gat gat tta gtt gat tcc ctg aag ttt gca gtg ttg atg tgg gtg	3294
Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val	
1085 1090 1095	
ttt act tat gtt ggt gcc ttg ttc aat ggt ctg aca cta ctg att	3339
Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile	
1100 1105 1110	
tta gct ctg atc tca ctc ttc agt att cct gtt att tat gaa cgg	3384
Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg	
1115 1120 1125	
cat cag gtg cag ata gat cat tat cta gga ctt gca aac aag agt	3429

His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser  
 1130 1135 1140

gtt aag gat gcc atg gcc aaa atc caa gca aaa atc cct gga ttg 3474  
 Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu  
 1145 1150 1155

aag cgc aaa gca gat tga 3492  
 Lys Arg Lys Ala Asp  
 1160

<210> 26  
 <211> 1163  
 <212> PRT  
 <213> Rattus norvegicus

<400> 26

Met Glu Asp Ile Asp Gln Ser Ser Leu Val Ser Ser Ser Thr Asp Ser  
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Pro Pro Arg Pro Pro Pro Ala Phe Lys Tyr Gln Phe Val Thr Glu Pro  
 20 25 30

Glu Asp Glu Glu Asp Glu Glu Glu Glu Glu Asp Glu Glu Glu Asp Asp  
 35 40 45

Glu Asp Leu Glu Glu Leu Glu Val Leu Glu Arg Lys Pro Ala Ala Gly  
 50 55 60

Leu Ser Ala Ala Ala Val Pro Pro Ala Ala Ala Ala Pro Leu Leu Asp  
 65 70 75 80

Phe Ser Ser Asp Ser Val Pro Pro Ala Pro Arg Gly Pro Leu Pro Ala  
 85 90 95

Ala Pro Pro Ala Ala Pro Glu Arg Gln Pro Ser Trp Glu Arg Ser Pro  
 100 105 110

Ala Ala Pro Ala Pro Ser Leu Pro Pro Ala Ala Ala Val Leu Pro Ser  
 115 120 125

Lys Leu Pro Glu Asp Asp Glu Pro Pro Ala Arg Pro Pro Pro Pro Pro  
 130 135 140

Pro Ala Gly Ala Ser Pro Leu Ala Glu Pro Ala Ala Pro Pro Ser Thr  
 145 150 155 160

Pro Ala Ala Pro Lys Arg Arg Gly Ser Gly Ser Val Asp Glu Thr Leu  
 165 170 175

Phe Ala Leu Pro Ala Ala Ser Glu Pro Val Ile Pro Ser Ser Ala Glu  
 180 185 190

Lys Ile Met Asp Leu Met Glu Gln Pro Gly Asn Thr Val Ser Ser Gly  
 195 200 205

Gln Glu Asp Phe Pro Ser Val Leu Leu Glu Thr Ala Ala Ser Leu Pro  
 210 215 220

Ser Leu Ser Pro Leu Ser Thr Val Ser Phe Lys Glu His Gly Tyr Leu  
 225 230 235 240

Gly Asn Leu Ser Ala Val Ser Ser Ser Glu Gly Thr Ile Glu Glu Thr  
 245 250 255

Leu Asn Glu Ala Ser Lys Glu Leu Pro Glu Arg Ala Thr Asn Pro Phe  
 260 265 270

Val Asn Arg Asp Leu Ala Glu Phe Ser Glu Leu Glu Tyr Ser Glu Met  
 275 280 285

Gly Ser Ser Phe Lys Gly Ser Pro Lys Gly Glu Ser Ala Ile Leu Val  
 290 295 300

Glu Asn Thr Lys Glu Glu Val Ile Val Arg Ser Lys Asp Lys Glu Asp  
 305 310 315 320

Leu Val Cys Ser Ala Ala Leu His Ser Pro Gln Glu Ser Pro Val Gly  
 325 330 335

Lys Glu Asp Arg Val Val Ser Pro Glu Lys Thr Met Asp Ile Phe Asn  
 340 345 350

Glu Met Gln Met Ser Val Val Ala Pro Val Arg Glu Glu Tyr Ala Asp  
 355 360 365

Phe Lys Pro Phe Glu Gln Ala Trp Glu Val Lys Asp Thr Tyr Glu Gly  
 370 375 380

Ser Arg Asp Val Leu Ala Ala Arg Ala Asn Val Glu Ser Lys Val Asp  
 385 390 395 400

Arg Lys Cys Leu Glu Asp Ser Leu Glu Gln Lys Ser Leu Gly Lys Asp  
 405 410 415

Ser Glu Gly Arg Asn Glu Asp Ala Ser Phe Pro Ser Thr Pro Glu Pro  
 420 425 430

Val Lys Asp Ser Ser Arg Ala Tyr Ile Thr Cys Ala Ser Phe Thr Ser  
 435 440 445

Ala Thr Glu Ser Thr Thr Ala Asn Thr Phe Pro Leu Leu Glu Asp His  
 450 455 460

Thr Ser Glu Asn Lys Thr Asp Glu Lys Lys Ile Glu Glu Arg Lys Ala  
 465 470 475 480

Gln Ile Ile Thr Glu Lys Thr Ser Pro Lys Thr Ser Asn Pro Phe Leu  
 485 490 495

Val Ala Val Gln Asp Ser Glu Ala Asp Tyr Val Thr Thr Asp Thr Leu  
 500 505 510

Ser Lys Val Thr Glu Ala Ala Val Ser Asn Met Pro Glu Gly Leu Thr  
 515 520 525

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr  
 530 535 540

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser  
 545 550 555 560

Glu Ala Ile Gln Glu Ser Leu Tyr Pro Thr Ala Gln Leu Cys Pro Ser  
 565 570 575

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val  
 580 585 590

Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val  
 595 600 605

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr  
 610 615 620

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala  
 625 630 635 640

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu  
 645 650 655

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile  
 660 665 670

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro  
 675 680 685

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser  
 690 695 700

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu  
705 710 715 720  
Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr  
725 730 735  
Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val Ser  
740 745 750  
Glu Thr Val Ala Gln His Lys Glu Glu Arg Leu Ser Ala Ser Pro Gln  
755 760 765  
Glu Leu Gly Lys Pro Tyr Leu Glu Ser Phe Gln Pro Asn Leu His Ser  
770 775 780  
Thr Lys Asp Ala Ala Ser Asn Asp Ile Pro Thr Leu Thr Lys Lys Glu  
785 790 795 800  
Lys Ile Ser Leu Gln Met Glu Glu Phe Asn Thr Ala Ile Tyr Ser Asn  
805 810 815  
Asp Asp Leu Leu Ser Ser Lys Glu Asp Lys Ile Lys Glu Ser Glu Thr  
820 825 830  
Phe Ser Asp Ser Ser Pro Ile Glu Ile Ile Asp Glu Phe Pro Thr Phe  
835 840 845  
Val Ser Ala Lys Asp Asp Ser Pro Lys Leu Ala Lys Glu Tyr Thr Asp  
850 855 860  
Leu Glu Val Ser Asp Lys Ser Glu Ile Ala Asn Ile Gln Ser Gly Ala  
865 870 875 880  
Asp Ser Leu Pro Cys Leu Glu Leu Pro Cys Asp Leu Ser Phe Lys Asn  
885 890 895  
Ile Tyr Pro Lys Asp Glu Val His Val Ser Asp Glu Phe Ser Glu Asn  
900 905 910  
Arg Ser Ser Val Ser Lys Ala Ser Ile Ser Pro Ser Asn Val Ser Ala  
915 920 925  
Leu Glu Pro Gln Thr Glu Met Gly Ser Ile Val Lys Ser Lys Ser Leu  
930 935 940  
Thr Lys Glu Ala Glu Lys Lys Leu Pro Ser Asp Thr Glu Lys Glu Asp  
945 950 955 960  
Arg Ser Leu Ser Ala Val Leu Ser Ala Glu Leu Ser Lys Thr Ser Val

965

970

975

Val Asp Leu Leu Tyr Trp Arg Asp Ile Lys Lys Thr Gly Val Val Phe  
 980 985 990

Gly Ala Ser Leu Phe Leu Leu Leu Ser Leu Thr Val Phe Ser Ile Val  
 995 1000 1005

Ser Val Thr Ala Tyr Ile Ala Leu Ala Leu Leu Ser Val Thr Ile  
 1010 1015 1020

Ser Phe Arg Ile Tyr Lys Gly Val Ile Gln Ala Ile Gln Lys Ser  
 1025 1030 1035

Asp Glu Gly His Pro Phe Arg Ala Tyr Leu Glu Ser Glu Val Ala  
 1040 1045 1050

Ile Ser Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly  
 1055 1060 1065

His Val Asn Ser Thr Ile Lys Glu Leu Arg Arg Leu Phe Leu Val  
 1070 1075 1080

Asp Asp Leu Val Asp Ser Leu Lys Phe Ala Val Leu Met Trp Val  
 1085 1090 1095

Phe Thr Tyr Val Gly Ala Leu Phe Asn Gly Leu Thr Leu Leu Ile  
 1100 1105 1110

Leu Ala Leu Ile Ser Leu Phe Ser Ile Pro Val Ile Tyr Glu Arg  
 1115 1120 1125

His Gln Val Gln Ile Asp His Tyr Leu Gly Leu Ala Asn Lys Ser  
 1130 1135 1140

Val Lys Asp Ala Met Ala Lys Ile Gln Ala Lys Ile Pro Gly Leu  
 1145 1150 1155

Lys Arg Lys Ala Asp  
 1160

<210> 27  
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 <212> PRT  
 <213> Rattus norvegicus

<220>  
 <221> PEPTIDE  
 <222> (1)..(25)  
 <223> rat PEP4

<400> 27

Glu Glu Leu Val Gln Lys Tyr Ser Asn Ser Ala Leu Gly His Val Asn  
1 5 10 15

Ser Thr Ile Lys Glu Leu Arg Arg Leu  
20 25

<210> 28

<211> 17

<212> PRT

<213> Artificial Sequence

<220>

<223> PRO/SER rich peptide

<220>

<221> PEPTIDE

<222> (1)..(17)

<223> Synthetic peptide

<400> 28

Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro Ser Ser Pro Pro Pro  
1 5 10 15

Ser

<210> 29

<211> 25

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-2F

<220>

<221> primer\_bind

<222> (1)..(25)

<223> CA-NA-2F primer

<400> 29

aagcaccatt gaattctgca gttcc

25

<210> 30

<211> 28

<212> DNA

<213> Artificial Sequence

<220>

<223> CA-NA-3R

<220>

<221> primer\_bind

<222> (1)..(28)



<400> 30  
aactgcagta ctgagctcct ccattctgc 28

<210> 31  
<211> 33  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> forward 5'

<220>  
<221> primer\_bind  
<222> (1)..(33)  
<223> forward primer

<400> 31  
gtcgcggatc catggagacc ctttttgctc ttc 33

<210> 32  
<211> 27  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> reverse 5'

<220>  
<221> primer\_bind  
<222> (1)..(27)  
<223> reverse primer

<400> 32  
gttctcgagt tatgaagttt tactcag 27

<210> 33  
<211> 29  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> forward 5'-1

<220>  
<221> primer\_bind  
<222> (1)..(29)  
<223> primer

<400> 33  
gtgcggatcc atggatttga aggagcagc 29

<210> 34  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>

<223> reverse 5'-1

<220>

<221> primer\_bind

<222> (1)..(28)

<223> primer

<400> 34

gtttctcgag tgaagtttta ttcagctc

28

<210> 35

<211> 20

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' primer

<220>

<221> primer\_bind

<222> (1)..(20)

<223> primer

<400> 35

tccaccccg cgcgcgcca

20

<210> 36

<211> 22

<212> DNA

<213> Artificial Sequence

<220>

<223> 5' primer 2

<220>

<221> primer\_bind

<222> (1)..(22)

<223> primer

<400> 36

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22

<210> 37

<211> 24

<212> DNA

<213> Artificial Sequence

<220>

<223> 3' primer

<220>

<221> primer\_bind

<222> (1)..(24)

<223> primer

<400> 37

ggtacaaaga ttgcttatga aaca

24

<210> 38  
<211> 22  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3' primer 2

<220>  
<221> primer\_bind  
<222> (1)..(22)  
<223> primer

<400> 38  
agcagggcca aggcaatgta gg

22

<210> 39  
<211> 28  
<212> DNA  
<213> Artificial Sequence

<220>  
<223> 5'-VL leader

<220>  
<221> primer\_bind  
<222> (1)..(28)  
<223> primer

<400> 39  
aatatgagtc ctgcccagtt cctgtttc

28

<210> 40  
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<212> DNA  
<213> Artificial Sequence

<220>  
<223> 3'-Ck

<220>  
<221> primer\_bind  
<222> (1)..(32)  
<223> primer

<400> 40  
ttaggaattc ctaacactct cccctgttga ag

32

<210> 41  
<211> 31  
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<220>  
<223> 5'-VH leader

<220>

<221> primer\_bind  
 <222> (1)..(31)  
 <223> primer  
  
 <400> 41  
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 <210> 42  
 <211> 24  
 <212> DNA  
 <213> Artificial Sequence  
  
 <220>  
 <223> 3'-CH hinge  
  
 <220>  
 <221> primer\_bind  
 <222> (1)..(24)  
 <223> primer  
  
 <400> 42  
 aattgggcaa cgttgcaggt gacg 24  
  
 <210> 43  
 <211> 663  
 <212> DNA  
 <213> Mus musculus  
  
 <220>  
 <221> misc\_binding  
 <222> (1)..(663)  
 <223> DNA variable part of heavy chain 11C7  
  
 <400> 43  
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 aagcttctcg agtctggagg tggcctggtg cagcctggag gatccctgaa actctcctgt 120  
 gtagtctcag gattcgattt tagaagaaat tggatgagtt ggggccggca ggctcctggg 180  
 aaagggctag aatggatttg agaaattaat ccagatagca gtaagataaa ctatacgcca 240  
 tctctaaagg ataaattcat catctccaga gacaatgcca agaatacgct gtacctgcaa 300  
 gtgagcacag tgagatctga ggacacagcc ctttattact gtgtgagacc ggtctggatg 360  
 tatgctatgg actactgggg tcaaggaacc tcagtcaccg tctcctcagc caaaacgaca 420  
 ccccatctg tctatccact ggcccctgga tctgctgccc aaactaactc catggtgacc 480  
 ctgggatgcc tgggtcaagg ctatttcctt gagccagtga cagtgcctg gaactctgga 540  
 tccctgtcca gcggtgtgca caccttccca gctgtcctgc agtctgacct ctacactctg 600  
 agcagctcag tgactgtccc ctccagcacc tggcccagcg agaccgtcac ctgcaacggt 660  
 gcc 663  
  
 <210> 44  
 <211> 717

<212> DNA  
<213> Mus musculus

<220>  
<221> misc\_binding  
<222> (1)..(717)  
<223> variable part of light chain of 11C7

<400> 44  
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gttctgtttga cccagactcc tctcactttg tcgataacca ttggacaacc agcctccatc 120  
tcttgcaagt caagtcagag cctcttgcac agtgatggaa agacatatat gaattgggttg 180  
ttacagagggc caggccagtc tccaaagcgc ctaatctatc tgggtgtctaa actggactct 240  
ggagtcacctg acaggttcac tggcagtggg tcagggacgg atttcacact gaaaatcagc 300  
agagtggagg ctgaggattt gggactttat tattgctggc aaggtacaca ttttcctcag 360  
acgttcggtg gaggcaccaa gctggaaatc aaacgggctg atgctgcacc aactgtatcc 420  
atcttccac catccagtga gcagttaaca tctggagggtg cctcagtcgt gtgcttcttg 480  
aacaacttct accccaaaga catcaatgtc aagtggaaga ttgatggcag tgaacgacaa 540  
aatggcgctc tgaacagttg gactgatcag gacagcaaag acagcaccta cagcatgagc 600  
agcaccctca cgttgaccaa ggacgagtat gaacgacata acagctatac ctgtgaggcc 660  
actcacaaga catcaacttc acccattgtc aagagcttca acaggggaga gtgttag 717

<210> 45  
<211> 239  
<212> PRT  
<213> Homo sapiens

<400> 45

Thr Lys Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr  
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Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr  
20 25 30

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser  
35 40 45

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser  
50 55 60

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val  
65 70 75 80

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Val  
85 90 95

Ile Gln Pro Ser Ser Ser Pro Leu Glu Ala Ser Ser Val Asn Tyr Glu  
100 105 110

Ser Ile Lys His Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala Met  
115 120 125

Ser Val Ser Leu Lys Lys Val Ser Gly Ile Lys Glu Glu Ile Lys Glu  
130 135 140

Pro Glu Asn Ile Asn Ala Ala Leu Gln Glu Thr Glu Ala Pro Tyr Ile  
145 150 155 160

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Ala Glu Pro  
165 170 175

Ala Pro Asp Phe Ser Asp Tyr Ser Glu Met Ala Lys Val Glu Gln Pro  
180 185 190

Val Pro Asp His Ser Glu Leu Val Glu Asp Ser Ser Pro Asp Ser Glu  
195 200 205

Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Asp Val Pro Gln Lys  
210 215 220

Gln Asp Glu Thr Val Met Leu Val Lys Glu Ser Leu Thr Glu Thr  
225 230 235

<210> 46  
<211> 239  
<212> PRT  
<213> Pan paniscus

<400> 46

Gly Lys Val Thr Glu Glu Val Val Ala Asn Met Pro Glu Gly Leu Thr  
1 5 10 15

Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Val Thr  
20 25 30

Gly Thr Lys Ile Ala Tyr Glu Thr Lys Met Asp Leu Val Gln Thr Ser  
35 40 45

Glu Val Met Gln Glu Ser Leu Tyr Pro Ala Ala Gln Leu Cys Pro Ser  
50 55 60

Phe Glu Glu Ser Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val  
65 70 75 80

Met Glu Ala Pro Leu Asn Ser Ala Val Pro Ser Ala Gly Ala Ser Ala

	85		90		95										
Val	Gln	Pro	Ser	Ser	Ser	Pro	Leu	Glu	Ala	Ser	Ser	Val	Asn	Tyr	Glu
			100					105					110		
Ser	Ile	Ile	His	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala	Met
		115					120					125			
Ser	Val	Ser	Leu	Lys	Lys	Val	Ser	Gly	Ile	Lys	Glu	Glu	Ile	Lys	Glu
	130					135					140				
Pro	Glu	Ser	Ile	Asn	Ala	Ala	Val	Gln	Glu	Thr	Glu	Ala	Pro	Tyr	Ile
145					150					155					160
Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Ala	Glu	Pro
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Thr	Pro	Asp	Phe	Ser	Asp	Tyr	Ser	Glu	Met	Ala	Lys	Val	Glu	Gln	Pro
			180					185					190		
Val	Pro	Asp	His	Ser	Glu	Leu	Val	Glu	Asp	Ser	Ser	Pro	Asp	Ser	Glu
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		35					40					45			
Glu	Ala	Ile	Gln	Glu	Ser	Leu	Tyr	Pro	Thr	Ala	Gln	Leu	Cys	Pro	Ser
	50					55					60				
Phe	Glu	Glu	Ala	Glu	Ala	Thr	Pro	Ser	Pro	Val	Leu	Pro	Asp	Ile	Val
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Met Glu Ala Pro Leu Asn Ser Leu Leu Pro Ser Ala Gly Ala Ser Val  
85 90 95

Val Gln Pro Ser Val Ser Pro Leu Glu Ala Pro Pro Pro Val Ser Tyr  
100 105 110

Asp Ser Ile Lys Leu Glu Pro Glu Asn Pro Pro Pro Tyr Glu Glu Ala  
115 120 125

Met Asn Val Ala Leu Lys Ala Leu Gly Thr Lys Glu Gly Ile Lys Glu  
130 135 140

Pro Glu Ser Phe Asn Ala Ala Val Gln Glu Thr Glu Ala Pro Tyr Ile  
145 150 155 160

Ser Ile Ala Cys Asp Leu Ile Lys Glu Thr Lys Leu Ser Thr Glu Pro  
165 170 175

Ser Pro Asp Phe Ser Asn Tyr Ser Glu Ile Ala Lys Phe Glu Lys Ser  
180 185 190

Val Pro Glu His Ala Glu Leu Val Glu Asp Ser Ser Pro Glu Ser Glu  
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Pro Val Asp Leu Phe Ser Asp Asp Ser Ile Pro Glu Val Pro Gln Thr  
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Gln Glu Glu Ala Val Met Leu Met Lys Glu Ser Leu Thr Glu Val  
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Ser Lys Val Thr Glu Ala Val Val Ala Thr Met Pro Glu Gly Leu Thr  
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Pro Asp Leu Val Gln Glu Ala Cys Glu Ser Glu Leu Asn Glu Ala Thr  
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Gly Thr Lys Ile Ala Tyr Glu Thr Lys Val Asp Leu Val Gln Thr Ser  
35 40 45

Glu Ala Ile Gln Glu Ser Ile Tyr Pro Thr Ala Gln Leu Cys Pro Ser  
50 55 60

Phe Glu Glu Ala Glu Ala Thr Pro Ser Pro Val Leu Pro Asp Ile Val



65					70					75					80
Met	Glu	Ala	Pro	Leu	Asn	Ser	Leu	Leu	Pro	Ser	Thr	Gly	Ala	Ser	Val
				85					90					95	
Ala	Gln	Pro	Ser	Ala	Ser	Pro	Leu	Glu	Val	Pro	Ser	Pro	Val	Ser	Tyr
			100					105					110		
Asp	Gly	Ile	Lys	Leu	Glu	Pro	Glu	Asn	Pro	Pro	Pro	Tyr	Glu	Glu	Ala
		115					120					125			
Met	Ser	Val	Ala	Leu	Lys	Thr	Ser	Asp	Ser	Lys	Glu	Glu	Ile	Lys	Glu
	130					135					140				
Pro	Glu	Ser	Phe	Asn	Ala	Ala	Ala	Gln	Glu	Ala	Glu	Ala	Pro	Tyr	Ile
145					150					155					160
Ser	Ile	Ala	Cys	Asp	Leu	Ile	Lys	Glu	Thr	Lys	Leu	Ser	Thr	Glu	Pro
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225					230					235					